

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/528,708  
Source: PJ  
Date Processed by STIC: 3/30/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/528,708

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics  
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino  
Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0  
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences  
(OLD RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences  
(NEW RULES)** Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ **Use of n's or Xaa's  
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>  
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0  
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005

TIME: 14:13:00

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

3 <110> APPLICANT: Stiftung Alfred-Wegener-Institut fuer Polar- und  
 4 Meeresforschung,  
 5 Bremerhaven, Germany  
 7 <120> TITLE OF INVENTION: A novel nucleic acid sequence coding for a calpain  
 8 protease from the coldness-adapted marine fragilariopsis  
 9 cylindrus diatom  
 11 <130> FILE REFERENCE: AWI 01/0902 DE  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,708  
 C--> 13 <141> CURRENT FILING DATE: 2005-03-22  
 13 <160> NUMBER OF SEQ ID NOS: 4

*pp-1-b*  
*see item 4*  
*on Error Summary*  
*Sheet*

## ERRORED SEQUENCES

*Does Not Comply*  
*Corrected Diskette Needed*

15 <210> SEQ ID NO: 1  
 16 <211> LENGTH: 544  
 17 <212> TYPE: DNA  
 18 <213> ORGANISM: Fragilariopsis cylindrus  
 20 <400> SEQUENCE: 1  
 E--> 22 gg gaa ttc ggc ctt acg gcc ggg gat gat gga atg ttc tgg att  
 23 agt 47  
 24 Glu Phe Gly Leu Thr Ala Gly Asp Asp Gly Met Phe Trp Ile  
 W--> 25 Ser  
 W--> 26 1 5 10  
 E--> 27 15  
 E--> 29 tgg gag gat gtc ttg ctt tat ttc cgc aat tta caa tta tca tgg  
 30 aat 95  
 31 Trp Glu Asp Val Leu Leu Tyr Phe Arg Asn Leu Gln Leu Ser Trp  
 W--> 32 Asn  
 W--> 33 20 25 30  
 E--> 35 ccc aaa cta ttt gcg tat cgg atg act act cat ggc tta tgg cca  
 36 aag 143  
 37 Pro Lys Leu Phe Ala Tyr Arg Met Thr Thr His Gly Leu Trp Pro  
 W--> 38 Lys  
 W--> 39 35 40 45  
 E--> 41 gat cag gga cca caa aat gat gca ttt aat gtc gga gag aat cca  
 42 caa 191  
 43 Asp Gln Gly Pro Gln Asn Asp Ala Phe Asn Val Gly Glu Asn Pro  
 W--> 44 Gln  
 W--> 45 50 55 60  
 E--> 47 tat atc atg tct ttc tcc gaa aaa gct gta tgg agt aaa cca acg  
 48 att 239  
 49 Tyr Ile Met Ser Phe Ser Glu Lys Ala Val Ser Ser Lys Pro Thr

*see item 1*  
*on Error*  
*Summary*  
*Sheet*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005

TIME: 14:13:00

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

```

W--> 50 Ile
W--> 51      65      70      75
E--> 53 tgg gta ctg ata tca agg cat gta agc aaa cag gag caa gaa ggt
      54 gct      287
      55 Trp Val Leu Ile Ser Arg His Val Ser Lys Gln Glu Gln Glu Gly
W--> 56 Ala
W--> 57 80      85      90
E--> 58 95
E--> 60 gag gtg aat gat ttc tta acc ata cat ctc gtt aga aac tcg gct
      61 aca      335
      62 Glu Val Asn Asp Phe Leu Thr Ile His Leu Val Arg Asn Ser Ala
W--> 63 Thr
W--> 64      100      105      110
E--> 66 tta gaa aga gtt tgg tat ccc cat gga aaa gca acg att gct aat
      67 gga      383
      68 Leu Glu Arg Val Trp Tyr Pro His Gly Lys Ala Thr Ile Ala Asn
W--> 69 Gly
W--> 72      115      120      125
E--> 74 tgc tat aca aac aat cca cac gtg ctt tta cga tac gat gtt tcc
      75 gga      431
      76 Cys Tyr Thr Asn Asn Pro His Val Leu Leu Arg Tyr Asp Val Ser
W--> 77 Gly
W--> 78      130      135      140
E--> 80 cct gaa gat caa ttt atc tcg tta gta ctg tct caa cac gaa aaa
      81 act      479
      82 Pro Glu Asp Gln Phe Ile Ser Leu Val Leu Ser Gln His Glu Lys
W--> 83 Thr
W--> 84      145      150      155
E--> 86 caa gat cta tca tac act ctc tct tgt tac tgt acc gaa ccc ttt
      87 aca      527
      88 Gln Asp Leu Ser Tyr Thr Leu Ser Cys Tyr Cys Thr Glu Pro Phe
W--> 89 Thr
W--> 90 160      165      170
E--> 91 175
E--> 93 cta gga aga cca cca aa
      94      544
      95 Leu Gly Arg Pro Pro
W--> 96      180
      99 <210> SEQ ID NO: 2
      100 <211> LENGTH: 180
      101 <212> TYPE: DNA
      102 <213> ORGANISM: Fragilariopsis cylindrus
      104 <400> SEQUENCE: 2
      105      Glu Phe Gly Leu Thr Ala Gly Asp Asp Gly Met Phe Trp Ile
W--> 106 Ser
W--> 107      1      5      10
E--> 108 15
      110 Trp Glu Asp Val Leu Leu Tyr Phe Arg Asn Leu Gln Leu Ser Trp
W--> 111 Asn

```

*see item 1  
on Euro  
summary sheet*

*see item 1*

## RAW SEQUENCE LISTING

DATE: 03/30/2005

PATENT APPLICATION: US/10/528,708

TIME: 14:13:00

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

```

W--> 112          20          25          30
      114 Pro Lys Leu Phe Ala Tyr Arg Met Thr Thr His Gly Leu Trp Pro
W--> 115 Lys
W--> 116          35          40          45
      118 Asp Gln Gly Pro Gln Asn Asp Ala Phe Asn Val Gly Glu Asn Pro
W--> 119 Gln
W--> 120          50          55          60
      122 Tyr Ile Met Ser Phe Ser Glu Lys Ala Val Ser Ser Lys Pro Thr
W--> 123 Ile
W--> 124          65          70          75
      126 Trp Val Leu Ile Ser Arg His Val Ser Lys Gln Glu Gln Glu Gly
W--> 127 Ala
W--> 128 80          85          90
E--> 129 95
      131 Glu Val Asn Asp Phe Leu Thr Ile His Leu Val Arg Asn Ser Ala
W--> 132 Thr
W--> 133          100          105          110
      135 Leu Glu Arg Val Trp Tyr Pro His Gly Lys Ala Thr Ile Ala Asn
W--> 136 Gly
W--> 137          115          120          125
      141 Cys Tyr Thr Asn Asn Pro His Val Leu Leu Arg Tyr Asp Val Ser
W--> 142 Gly
W--> 143          130          135          140
      145 Pro Glu Asp Gln Phe Ile Ser Leu Val Leu Ser Gln His Glu Lys
W--> 146 Thr
W--> 147          145          150          155
      149 Gln Asp Leu Ser Tyr Thr Leu Ser Cys Tyr Cys Thr Glu Pro Phe
W--> 150 Thr
W--> 151 160          165          170
E--> 152 175
      154 Leu Gly Arg Pro Pro
E--> 155          180
      159 <210> SEQ ID NO: 3
      160 <211> LENGTH: 544
      161 <212> TYPE: DNA
      162 <213> ORGANISM: Fragilariopsis cylindrus
      164 <400> SEQUENCE: 3
E--> 166 tca aac gat ggt gcg caa tac gta gta gag aaa tcg ata ctg gta
      167 ggt 48
      168 Ser Asn Asp Gly Ala Gln Tyr Val Val Glu Lys Ser Ile Leu Val
W--> 169 Gly
W--> 170 1 5 10 15
E--> 172 tca gtg aat tat cct gta aaa gat cca ttt aat cag atg aaa cgt
      173 gga 96
      174 Ser Val Asn Tyr Pro Val Lys Asp Pro Phe Asn Gln Met Lys Arg
W--> 175 Gly
W--> 176          20          25          30
E--> 178 tca ctt caa acc tac tca gat tca tgg acc gaa cgg gat cgt acc
      179 tca 144

```

*see  
item 1*

*see  
item 1*

## RAW SEQUENCE LISTING

DATE: 03/30/2005

PATENT APPLICATION: US/10/528,708

TIME: 14:13:00

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

```

180 Ser Leu Gln Thr Tyr Ser Asp Ser Trp Thr Glu Arg Asp Arg Thr
W--> 181 Ser
W--> 182          35          40          45
E--> 184 ttt gtc atg gca tca cgt aac tta gcc gat ttt cgt aat aac gtg
185 aag 192
186 Phe Val Met Ala Ser Arg Asn Leu Ala Asp Phe Arg Asn Asn Val
W--> 187 Lys
W--> 188          50          55          60
E--> 190 gta acg atc gat gct gtt ttt aat cca ctt ttt atc aac gag gaa
191 tac 240
192 Val Thr Ile Asp Ala Val Phe Asn Pro Leu Phe Ile Asn Glu Glu
W--> 193 Tyr
W--> 194 65          70          75
E--> 195 80
E--> 197 aaa tgg atc ttt cgt caa gaa ggc tgg agg tta gag aca cct gac
198 aat 288
199 Lys Trp Ile Phe Arg Gln Glu Gly Trp Arg Leu Glu Thr Pro Asp
W--> 200 Asn
W--> 201          85          90          95
E--> 203 gtc aac cta ctt atc aat ggg aac gct tat gta aac gct aag gcc
204 gac 336
205 Val Asn Leu Leu Ile Asn Gly Asn Ala Tyr Val Asn Ala Lys Ala
W--> 206 Asp
W--> 207          100          105          110
E--> 211 cag atg gac ccc caa gag gtt atg ata aag caa atc tac agc aat
212 ctc 384
213 Gln Met Asp Pro Gln Glu Val Met Ile Lys Gln Ile Tyr Ser Asn
W--> 214 Leu
W--> 215          115          120          125
E--> 217 ttt gct gat cac gtg tat agc aaa agt cca aaa gga gac gcc gcc
218 caa 432
219 Phe Ala Asp His Val Tyr Ser Lys Ser Pro Lys Gly Asp Ala Ala
W--> 220 Gln
W--> 221          130          135          140
E--> 223 gta gtc acc atg aca ttg gca cca agg gcg aat tct gca gat atc
224 cat 480
225 Val Val Thr Met Thr Leu Ala Pro Arg Ala Asn Ser Ala Asp Ile
W--> 226 His
W--> 227 145          150          155
E--> 228 160
E--> 230 cac act ggc ggc cgt ctc gag cat gca tct aga ggg ccc aat tcg
231 ccc 528
232 His Thr Gly Gly Arg Leu Glu His Ala Ser Arg Gly Pro Asn Ser
W--> 233 Pro
W--> 234          165          170          175
E--> 236 tat agt gag tcg tat t
237 544
238 Tyr Ser Glu Ser Tyr
W--> 239          180 181

```

*see  
item 1*

*← delete (insert amino acid number  
under every 5 amino acids)*

## RAW SEQUENCE LISTING

DATE: 03/30/2005

PATENT APPLICATION: US/10/528,708

TIME: 14:13:00

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

242 <210> SEQ ID NO: 4  
 243 <211> LENGTH: 181  
 244 <212> TYPE: DNA  
 245 <213> ORGANISM: Fragilariopsis cylindrus  
 247 <400> SEQUENCE: 4  
 249 Ser Asn Asp Gly Ala Gln Tyr Val Val Glu Lys Ser Ile Leu Val  
 W--> 250 Gly  
 W--> 251 1 5 10 15  
 253 Ser Val Asn Tyr Pro Val Lys Asp Pro Phe Asn Gln Met Lys Arg  
 W--> 254 Gly  
 W--> 255 20 25 30  
 257 Ser Leu Gln Thr Tyr Ser Asp Ser Trp Thr Glu Arg Asp Arg Thr  
 W--> 258 Ser  
 W--> 259 35 40 45  
 261 Phe Val Met Ala Ser Arg Asn Leu Ala Asp Phe Arg Asn Asn Val  
 W--> 262 Lys  
 W--> 263 50 55 60  
 265 Val Thr Ile Asp Ala Val Phe Asn Pro Leu Phe Ile Asn Glu Glu  
 W--> 266 Tyr  
 W--> 267 65 70 75  
 E--> 268 80  
 270 Lys Trp Ile Phe Arg Gln Glu Gly Trp Arg Leu Glu Thr Pro Asp  
 W--> 271 Asn  
 W--> 272 85 90 95  
 274 Val Asn Leu Leu Ile Asn Gly Asn Ala Tyr Val Asn Ala Lys Ala  
 W--> 275 Asp  
 W--> 276 100 105 110  
 280 Gln Met Asp Pro Gln Glu Val Met Ile Lys Gln Ile Tyr Ser Asn  
 W--> 281 Leu  
 W--> 282 115 120 125  
 284 Phe Ala Asp His Val Tyr Ser Lys Ser Pro Lys Gly Asp Ala Ala  
 W--> 285 Gln  
 W--> 286 130 135 140  
 288 Val Val Thr Met Thr Leu Ala Pro Arg Ala Asn Ser Ala Asp Ile  
 W--> 289 His  
 W--> 290 145 150 155  
 E--> 291 160  
 293 His Thr Gly Gly Arg Leu Glu His Ala Ser Arg Gly Pro Asn Ser  
 W--> 294 Pro  
 W--> 295 165 170 175  
 297 Tyr Ser Glu Ser Tyr  
 W--> 298 180 181  
 E--> 301 ~~Attorney Docket 050677-US~~

*see  
item 1*

*see p. 6 for more errors*

10/528,708 6

Sequence Protocol Listing

<110>Stiftung Alfred-Wegener-Institut fuer Polar- und  
Meeresforschung,  
Bremerhaven, Germany

<120>A novel nucleic acid sequence coding for a calpain  
protease from the coldness-adapted marine fragilariopsis  
cylindrus diatom

do not  
use  
italics

use a  
fixed-width font  
only

(per 1.823 of Sequence Rules)



# VERIFICATION SUMMARY

PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005

TIME: 14:13:01

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:22 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:1  
L:25 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
M:254 Repeated in SeqNo=1  
L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:33 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:108 M:254 E: No. of Bases conflict, this line has no nucleotides.  
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
M:254 Repeated in SeqNo=2  
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005

TIME: 14:13:01

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
 L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
 L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
 L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
 L:155 M:301 E: (44) No Sequence Data was Shown, SEQ ID:2  
 L:155 M:252 E: No. of Seq. differs, <211> LENGTH:Input:180 Found:0 SEQ:2  
 L:166 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:3  
 L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 M:254 Repeated in SeqNo=3  
 L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
 L:268 M:254 E: No. of Bases conflict, this line has no nucleotides.  
 M:254 Repeated in SeqNo=4  
 L:301 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3  
 L:301 M:301 E: (44) No Sequence Data was Shown, SEQ ID:4  
 L:301 M:252 E: No. of Seq. differs, <211> LENGTH:Input:181 Found:0 SEQ:4